

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/020,733

DATE: 01/10/2002

TIME: 15:52:03

Input Set : A:\LEX-0263-USA SEQLIST.txt  
 Output Set: N:\CRF3\01102002\J020733.raw

4 <110> APPLICANT: Walke, D. Wade  
 5 Wilganowski, Nathaniel L.  
 6 Friddle, Carl Johan  
 9 <120> TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same  
 11 <130> FILE REFERENCE: LEX-0263-USA  
**C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/020,733**  
**C--> 13 <141> CURRENT FILING DATE: 2001-10-30**  
 13 <150> PRIOR APPLICATION NUMBER: US 60/244,939  
 14 <151> PRIOR FILING DATE: 2000-11-01  
 16 <160> NUMBER OF SEQ ID NOS: 9  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 2781  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: homo sapiens  
 25 <400> SEQUENCE: 1

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27 cggccgggg cggcgccggga gcctggatgg acaagaggaa gtgaggaagg cagccccaaag	120
28 ctgcagcatg aacttatcat acctcagtgg aagacttcag aaagccccgt gagagaaaag	180
29 catccactca aagctgagct cagggtaatg gctgaggggc gagaactgtat cctggacctg	240
30 gagaagaatg agcaactttt tgctccatttc tacacagaaa cccattatac ttcaagtgg	300
31 aaccctcaaa ccaccacacg gaaattggag gatcactgt tttaccacgg cacggtgagg	360
32 gagacagaac tgtccagcgt caegctcagc acttggcagq gaatttagagg actgattacg	420
33 gtgagcagca acctcagcta cgtcatcagc cccctccctg acagcaaggg ccaacacctt	480
34 attacagat ctgaacatct caagccgccc cgggaaact gtgggttgcg gcactccaag	540
35 cccaccacca gggactgggc tcttcagttt acacaacaga ccaagaagcg acctcgcagg	600
36 atgaaaaggg aagatttaaa ctccatgaag tatgtggagc tttacctcggt ggctgattat	660
37 tttagagttc agaagaatcg acgagaccag gacgccccca aacacaagct catagagatc	720
38 gccaactatg ttgataagtt ttaccgatcc ttgaacatcc ggattgtct cgtggcttg	780
39 gaagtgtgga cccacgggaa catgtgtgaa gtttcagaga atccatattc taccctctgg	840
40 tcctttctca gttggaggcg caagctgctt gcccagaagt accatgacaa cggccaaatta	900
41 atcacgggca tgtccttcca cggcaccacc atcggctgg ccccccctcat gccatgtgc	960
42 tctgtgtacc agtctggagg agtcaacatg gaccactccg agaatgcccatttggctgg	1020
43 gccaccatgg cccacgagat gggccacaaac tttggcatga cccatgattc tgcagattgc	1080
44 tgctcggcca gtgcggctga tgggtgggtgc atcatggcag ctgcccactgg gcaccccttt	1140
45 cccaaagtgt tcaatggatg caacaggagg gagctggaca ggtatctgc gtcaggtgg	1200
46 ggaatgtgtc tctccaaacat gccagacacc aggatgttgt atggaggccg gaggtgtgg	1260
47 aacgggtatc tggaaagatgg ggaagagatgt gactgtggag aagaagagga atgtaaacaa	1320
48 ccctgctgca atgcctctaa ttgtaccctgtt agggccgggg cggagtgtgc tcacgctcc	1380
49 tgctgccacc agtgtaaatgt gtggctctt gggaccctgt gccgcgagca gcccaaggcag	1440
50 tggatggta cccctgtga gggcgcccgactgtatgc acaacggcat gtgcctcacc	1500
51 atggatggta cccctgtga gggcgcccgactgtatgc acaacggcat gtgcctcacc	1560
52 taccaggaggc agtgcacca gctgtggggc cccggagccc gacctggccc tgacccatgc	1620
53 ttccgagaagg tgaatgtggc agggacacc tttggaaact gtggaaaggg catgaatgg	1680
54 gaacacagga agtgcacca gggacacc tttggaaact gtggaaaggg catgaatgg	1740
55 gaggccggc ccctggagtc caacgcgggtg cccattgaca ccactatcat catgaatgg	1800
56 aggcagatcc agtgcgggg caccacgtc taccgaggc ctgaggagga gggtgacatg	1860

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57	ctggacccag	ggctggat	gactggacc	aagtgtggct	acaaccatat	ttgttttag	1920
58	ggcagtgc	gaaacacac	cttctttgaa	actgaaggct	gtggaaagaa	gtgcaatggc	1980
59	catggggct	gtacaacaa	ccagaactqc	cactgcctgc	cgggctgggc	cccccccttc	2040
60	tcaacacac	cggccacgg	ggcagtgatc	gacagtgggc	ctatgc	ttggatgtg	2100
61	gtcctgtgg	tagctggat	gttgggtggc	atcttggc	tggcggtct	catgtgtat	2160
62	tactactgt	gcagacagaa	caacaaacta	gcccaactca	agccctcagc	tctcccttcc	2220
63	aagctgagge	aacagttca	ttgtcccttc	agggttctc	agaacagegg	gactggat	2280
64	gccaacccaa	cttcaagct	gcagacgccc	caggcaagc	gaaagggttt	cattgacttg	2340
65	tgcgtacagg	tgtcaacac	tccggaaatc	ctgcgaaagc	cctcccgccc	tcetccccgg	2400
66	ccccctccag	attatctgcq	tgggggtcc	ccacctgcac	cactgccage	tcacctgagc	2460
67	aggctgtcta	ggaactcccc	aggggcccg	tctcaatag	agaggacgg	gtcgccagg	2520
68	aggctctc	caagccggcc	aattcccccc	gcaccaaatt	gatcgttt	ccaggactc	2580
69	tccaggcctc	ggccgccccca	gaaggcactc	ccggcaaacc	cagtgcagg	ccgcaggagc	2640
70	ctcccccaggc	caggaggtgc	atccccactg	cggcccttq	gtgctggccc	tcagcagtcc	2700
71	cgcctctgg	cagcaactgc	cccaaagagg	gtatgaa	tttgcattt	aaaaactggg	2760
72	gaccagttcc	aaagtca	ta				2781
74	<210>	SEQ ID NO:	2				
75	<211>	LENGTH:	926				
76	<212>	TYPE:	PRT				
77	<213>	ORGANISM:	homo sapiens				
79	<400>	SEQUENCE:	2				
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82	Leu Gln Pro	Leu Arg Pro	Arg Ala Ala Arg	Glu Pro	Gly Trp	Thr Arg	
83	20	25	30				
84	Gly Ser	Glu Glu	Gly Ser Pro	Lys Leu Gln	His Glu	Ile Ile Pro	
85	35	40	45				
86	Gln Trp Lys	Thr Ser Glu	Ser Pro Val	Arg Glu Lys	His Pro	Leu Lys	
87	50	55	60				
88	Ala Glu Leu	Arg Val Met	Ala Glu Gly	Arg Glu Leu	Ile Leu Asp	Leu	
89	65	70	75	80			
90	Glu Lys Asn	Glu Gln Leu	Phe Ala Pro	Ser Tyr Thr	Glu Thr His	Tyr	
91	85	90	95				
92	Thr Ser Ser	Gly Asn Pro	Gln Thr Thr	Arg Lys Leu	Glu Asp	His	
93	100	105	110				
94	Cys Phe Tyr	His Gly Thr	Val Arg Glu	Thr Glu Leu	Ser Ser	Val Thr	
95	115	120	125				
96	Leu Ser Thr	Cys Arg Gly	Ile Arg Gly	Leu Ile	Thr Val	Ser Ser Asn	
97	130	135	140				
98	Leu Ser Tyr	Val Ile Glu	Pro Leu Pro	Asp Ser Lys	Gly Gln	His Leu	
99	145	150	155	160			
100	Ile Tyr Arg	Ser Glu His	Leu Lys Pro	Pro Pro	Gly Asn Cys	Gly Phe	
101	165	170	175				
102	Glu His Ser	Lys Pro Thr	Thr Arg Asp	Trp Ala	Leu Gln	Phe Thr Gln	
103	180	185	190				
104	Gln Thr Lys	Lys Arg Pro	Arg Arg Met	Lys Arg Glu	Asp Leu	Asn Ser	
105	195	200	205				
106	Met Lys Tyr	Val Glu Leu	Tyr Leu Val	Ala Asp	Tyr Leu	Glu Phe Gln	
107	210	215	220				

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108	Lys Asn Arg Arg Asp Gln Asp Ala Thr Lys His Lys Leu Ile Glu Ile	
109 225	230	235 240
110	Ala Asn Tyr Val Asp Lys Phe Tyr Arg Ser Leu Asn Ile Arg Ile Ala	
111	245	250 255
112	Leu Val Gly Leu Glu Val Trp Thr His Gly Asn Met Cys Glu Val Ser	
113	260	265 270
114	Glu Asn Pro Tyr Ser Thr Leu Trp Ser Phe Leu Ser Trp Arg Arg Lys	
115	275	280 285
116	Leu Leu Ala Gln Lys Tyr His Asp Asn Ala Gln Leu Ile Thr Gly Met	
117	290	295 300
118	Ser Phe His Gly Thr Thr Ile Gly Leu Ala Pro Leu Met Ala Met Cys	
119 305	310	315 320
120	Ser Val Tyr Gln Ser Gly Gly Val Asn Met Asp His Ser Glu Asn Ala	
121	325	330 335
122	Ile Gly Val Ala Ala Thr Met Ala His Glu Met Gly His Asn Phe Gly	
123	340	345 350
124	Met Thr His Asp Ser Ala Asp Cys Cys Ser Ala Ser Ala Ala Asp Gly	
125	355	360 365
126	Gly Cys Ile Met Ala Ala Ala Thr Gly His Pro Phe Pro Lys Val Phe	
127	370	375 380
128	Asn Gly Cys Asn Arg Arg Glu Leu Asp Arg Tyr Leu Gln Ser Gly Gly	
129 385	390	395 400
130	Gly Met Cys Leu Ser Asn Met Pro Asp Thr Arg Met Leu Tyr Gly Gly	
131	405	410 415
132	Arg Arg Cys Gly Asn Gly Tyr Leu Glu Asp Gly Glu Glu Cys Asp Cys	
133	420	425 430
134	Gly Glu Glu Glu Cys Asn Asn Pro Cys Cys Asn Ala Ser Asn Cys	
135	435	440 445
136	Thr Leu Arg Pro Gly Ala Glu Cys Ala His Gly Ser Cys Cys His Gln	
137	450	455 460
138	Cys Lys Leu Leu Ala Pro Gly Thr Leu Cys Arg Glu Gln Ala Arg Gln	
139 465	470	475 480
140	Cys Asp Leu Pro Glu Phe Cys Thr Gly Lys Ser Pro His Cys Pro Thr	
141	485	490 495
142	Asn Phe Tyr Gln Met Asp Gly Thr Pro Cys Glu Gly Gly Gln Ala Tyr	
143	500	505 510
144	Cys Tyr Asn Gly Met Cys Leu Thr Tyr Gln Glu Gln Cys Gln Gln Leu	
145	515	520 525
146	Trp Gly Pro Gly Ala Arg Pro Ala Pro Asp Leu Cys Phe Glu Lys Val	
147	530	535 540
148	Asn Val Ala Gly Asp Thr Phe Gly Asn Cys Gly Lys Asp Met Asn Gly	
149 545	550	555 560
150	Glu His Arg Lys Cys Asn Met Arg Asp Ala Lys Cys Gly Lys Ile Gln	
151	565	570 575
152	Cys Gln Ser Ser Glu Ala Arg Pro Leu Glu Ser Asn Ala Val Pro Ile	
153	580	585 590
154	Asp Thr Thr Ile Ile Met Asn Gly Arg Gln Ile Gln Cys Arg Gly Thr	
155	595	600 605
156	His Val Tyr Arg Gly Pro Glu Glu Gly Asp Met Leu Asp Pro Gly	

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157	610	615	620
158	Leu Val Met Thr Gly Thr Lys Cys Gly Tyr Asn His Ile Cys Phe Glu		
159	625	630	635
160	Gly Gln Cys Arg Asn Thr Ser Phe Phe Glu Thr Glu Gly Cys Gly Lys		640
161	645	650	655
162	Lys Cys Asn Gly His Gly Val Cys Asn Asn Gln Asn Cys His Cys		
163	660	665	670
164	Leu Pro Gly Trp Ala Pro Pro Phe Cys Asn Thr Pro Gly His Gly Gly		
165	675	680	685
166	Ser Ile Asp Ser Gly Pro Met Pro Pro Glu Ser Val Gly Pro Val Val		
167	690	695	700
168	Ala Gly Val Leu Val Ala Ile Leu Val Leu Ala Val Leu Met Leu Met		
169	705	710	715
170	Tyr Tyr Cys Cys Arg Gln Asn Asn Lys Leu Gly Gln Leu Lys Pro Ser		720
171	725	730	735
172	Ala Leu Pro Ser Lys Leu Arg Gln Gln Phe Ser Cys Pro Phe Arg Val		
173	740	745	750
174	Ser Gln Asn Ser Gly Thr Gly His Ala Asn Pro Thr Phe Lys Leu Gln		
175	755	760	765
176	Thr Pro Gln Gly Lys Arg Lys Val Phe Leu Asp Leu Cys Val Gln Val		
177	770	775	780
178	Ile Asn Thr Pro Glu Ile Leu Arg Lys Pro Ser Gln Pro Pro Pro Arg		
179	785	790	795
180	Pro Pro Pro Asp Tyr Leu Arg Gly Gly Ser Pro Pro Ala Pro Leu Pro		800
181	805	810	815
182	Ala His Leu Ser Arg Ala Ala Arg Asn Ser Pro Gly Pro Gly Ser Gln		
183	820	825	830
184	Ile Glu Arg Thr Glu Ser Ser Arg Arg Pro Pro Pro Ser Arg Pro Ile		
185	835	840	845
186	Pro Pro Ala Pro Asn Cys Ile Val Ser Gln Asp Phe Ser Arg Pro Arg		
187	850	855	860
188	Pro Pro Gln Lys Ala Leu Pro Ala Asn Pro Val Pro Gly Arg Arg Ser		
189	865	870	875
190	Leu Pro Arg Pro Gly Gly Ala Ser Pro Leu Arg Pro Pro Gly Ala Gly		880
191	885	890	895
192	Pro Gln Gln Ser Arg Pro Leu Ala Ala Leu Ala Pro Lys Arg Val Trp		
193	900	905	910
194	Lys Thr Cys Asn Leu Lys Thr Gly Asp Gln Phe Gln Ser Gln		
195	915	920	925
197	<210> SEQ ID NO: 3		
198	<211> LENGTH: 2757		
199	<212> TYPE: DNA		
200	<213> ORGANISM: homo sapiens		
202	<400> SEQUENCE: 3		
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204	cggccgcggg cggcgccggga gcctggatgg acaagaggaa gtgaggaagg cagccccaaag		120
205	ctgcagcattg aacttatcat acctcagtgg aagacttcag aaagccccgt gagagaaaag		180
206	catccactca aagctgagct cagggtaatg qctgagggc gagaactgtat cctggacctg		240
207	gagaagaatg agcaacttt tgctccttcc tacacagaaa cccattatac ttcaagtgg		300

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208	aaccctcaaa	ccaccacacg	gaaattggag	gatcaactgct	tttaccacgg	cacggtgagg	360											
209	gagacagaac	tgtccagegt	cacgtcagc	acttgcgcag	gaatttagagg	actgattaa	420											
210	gtqagcagca	acctcagcta	cgtcatcgag	cccccccctg	acagaacagg	ccaacac	480											
211	atttacagat	ctgaacatct	caagccccc	ccggaaact	gtgggttcga	gcactccaag	540											
212	cccaccacca	gggactggc	tcttcagtt	acacaacaga	ccaagaagcg	acctcgca	600											
213	atgaaaagg	aaagattaaa	ctccatgaag	tatgtggagc	tttacctcgt	ggctgattat	660											
214	tttagagttc	agaagaatcg	acgagaccag	gacgccacca	aacacaagct	catagagato	720											
215	gccaactatg	ttgataagtt	ttaccgatcc	ttgaacatcc	ggattgctct	egtgggcttg	780											
216	gaagtgtgga	cccacggaa	catgtgtgaa	gttcagaga	atccatattc	tacccctetgg	840											
217	tcctttctca	gttggagge	caagctgctt	gcccagaatg	accatgacaa	cgcccaatta	900											
218	atcacgggca	tgtccttcca	gggcacacc	atcgccctgg	ccccctctat	ggccatgtgc	960											
219	tctgttacc	agtctggagg	agtcaacatg	gaccactccg	agaatgcac	tggcgtggct	1020											
220	gccaccatgg	cccacgagat	gggcacacaac	tttgcatga	cccatgatcc	tgcagattgc	1080											
221	tgctcggcca	gtgcgctga	ttgtgggtgc	atcatggcag	ctgccactgg	gcacccctt	1140											
222	cccaaagtgt	tcaatggatg	caacaggagg	gagctggaca	ggtatctgca	gtcaggttgt	1200											
223	qaaatgtgtc	tctccaaacat	ggcagacacc	aggatgttgt	atggaggccg	gagggtgtgg	1260											
224	aacgggtatc	ttgaagatgg	gaaagagtgt	gactgtggag	aagaagagga	atgtaaacaa	1320											
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234	ctggaccc	ggctgtgtat	gactggaa	aagtgttgt	acaaccat	ttgttttgay	1920											
235	ggcagtgc	ggaacac	ctt	tttgaa	actgaaggct	gtggaaagaa	gtcaatggc	1980										
236	catgggtct	gtaa	acacaa	ccagaactgc	cactgcctgc	cggtctggc	ccgccttc	2040										
237	tgcacac	cgggcac	gggcag	tac	gatggggc	ctatgcccc	tgagagtgt	2100										
238	gtcctgtgg	tagtgg	gttgg	atettgg	tggcgttct	catgtgtat	2160											
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240	aagctgaggc	aacat	ttc	agg	tttctc	agaacagcgg	gactgtgtat	2280										
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244	ccgggtctc	aaat	agag	gac	gg	gtc	ctccctca	2520										
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246	gactcccg	caa	accc	ca	ggc	act	ccaggccagg	2640										
247	ccactgcggc	ccc	ctgtt	gc	cc	cttgg	gac	acttgc	2700									
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253	<213>	ORGANISM:	homo sapiens															
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257	1				5			10			15							
258	L	e	u		u	u	u	u	u	u	u	u	u	u	u	u	u	u
	G	n			P	o		R	u	u	u	u	u	u	u	u	u	u

**VERIFICATION SUMMARY** DATE: 01/10/2002  
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Input Set : A:\LEX-0263-USA SEQLIST.txt  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date